

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WASTFALT, Maria K. Boden  
FLOCK, Jan-Ingmar
- (ii) TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
(B) STREET: P.O. Box 1404  
(C) CITY: Alexandria  
(D) STATE: Virginia  
(E) COUNTRY: United States  
(F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: TBA (Div of US 09/276,141)  
(B) FILING DATE: Even date herewith  
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/276,141  
(B) FILING DATE: 25-03-99  
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/244,229  
(B) FILING DATE: 09-DEC-1994  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: SE 9202720-0  
(B) FILING DATE: 21-SEP-1992
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: SE 9302955-1  
(B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: WO PCT/SE93/00759  
(B) FILING DATE: 20-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: McGowan, Malcolm K.

09530497 083704  
T.O. 230 2648550

- (B) REGISTRATION NUMBER: 39,300
- (C) REFERENCE/DOCKET NUMBER: 012889-011

- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 836-6620
  - (B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Asn Ser  
1                      5                      10                      15  
  
Lys Tyr Gly Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Lys Ser  
1                      5                      10                      15  
  
Lys Lys Gly Ala  
                    20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser  
1                      5                      10                      15  
  
Lys Asn Gly Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser  
1                      5                      10                      15  
  
Lys Asn Gly Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His  
1                      5                      10                      15  
  
Asn Ile Val Glu  
                    20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 8 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Pro Glu Lys Lys Pro Val  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCGAAGGA TACGGTCCAA GAGAAAAGAA ACCAGTGAGT ATTAATCACA ATATCGTAGA 60  
GTACAATGAT GGTACTTTTA AATATCAATC TAGACCAAAA TTAACTCAA CACCTAAATA 120  
TATTAAATTC AAACATGACT ATAATATTTT AGAATTTAAC GATGGTACAT TCGAATATGG 180  
TGCACGTCCA CAATTTAATA AACCAGCAGC GAAACTGAT GCAACTATTA AAAAAGAACA 240  
AAAATTGATT CAAGCTCAAA ATCTTGTGAG AGAATTTGAA AAAACACATA CTGTCAGTGC 300  
ACACAGAAAA GCACAAAAGG CAGTCAACTT AGTTTCGTTT GAATACAAAG TGAAGAAAAT 360  
GGTCTTACAA GAGCGAATTG ATAATGTATT AAAACAAGGA TTAGTGAG 408

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His  
1 5 10 15  
Asn Ile Val Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro  
20 25 30  
Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn  
35 40 45

Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln  
 50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln  
 65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His  
 85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser  
 100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn  
 115 120 125

Val Leu Lys Gln Gly Leu Val Arg  
 130 135

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 157..654

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 804..1007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTAGTGTA TAAGTGCTGA TGAGTCACAA GATAGATAAC TATATTTTGT CTATATTATA 60

AAGTGTTTAT AGTTAATTAA TAATTAGTTA ATTTCAAAAG TTGTATAAAAT AGGATAACTT 120

AATAAATGTA AGATAATAAT TTGGAGGATA ATTAAC ATG AAA AAT AAA TTG ATA 174  
 Met Lys Asn Lys Leu Ile  
 1 5

GCA AAA TCT TTA TTA ACA ATA GCG GCA ATT GGT ATT ACT ACA ACT ACA 222  
 Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile Gly Ile Thr Thr Thr Thr  
 10 15 20

ATT GCG TCA ACA GCA GAT GCG AGC GAA GGA TAC GGT CCA AGA GAA AAG 270  
 Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro Arg Glu Lys  
 25 30 35

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AAA CCA GTG AGT ATT AAT CAC AAT ATC GTA GAG TAC AAT GAT GGT ACT	318
Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn Asp Gly Thr	
40 45 50	
TTT AAA TAT CAA TCT AGA CCA AAA TTT AAC TCA ACA CCT AAA TAT ATT	366
Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro Lys Tyr Ile	
55 60 65 70	
AAA TTC AAA CAT GAC TAT AAT ATT TTA GAA TTT AAC GAT GGT ACA TTC	414
Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp Gly Thr Phe	
75 80 85	
GAA TAT GGT GCA CGT CCA CAA TTT AAT AAA CCA GCA GCG AAA ACT GAT	462
Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala Lys Thr Asp	
90 95 100	
GCA ACT ATT AAA AAA GAA CAA AAA TTG ATT CAA GCT CAA AAT CTT GTG	510
Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln Asn Leu Val	
105 110 115	
AGA GAA TTT GAA AAA ACA CAT ACT GTC AGT GCA CAC AGA AAA GCA CAA	558
Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg Lys Ala Gln	
120 125 130	
AAG GCA GTC AAC TTA GTT TCG TTT GAA TAC AAA GTG AAG AAA ATG GTC	606
Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys Lys Met Val	
135 140 145 150	
TTA CAA GAG CGA ATT GAT AAT GTA TTA AAA CAA GGA TTA GTG AGA TAA	654
Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu Val Arg *	
155 160 165	
TACTTCTGTC ATTATTTTAA GTTCAAATA ATTTAATATT ATATTATTTT TTATTAATAA	714
AACGACTATG CTATTTAATG CCAGGTAAAT GTAACCTTCC TAAAATTGAC TATATAATCG	774
TTAAGTATCA ATTTTAAGGA GAGTTTACA ATG AAA TTT AAA AAA TAT ATA TTA	827
Met Lys Phe Lys Lys Tyr Ile Leu	
1 5	
ACA GGA ACA TTA GCA TTA CTT TTA TCA TCA ACT GGG ATA GCA ACT ATA	875
Thr Gly Thr Leu Ala Leu Leu Leu Ser Ser Thr Gly Ile Ala Thr Ile	
10 15 20	
GAA GGG AAT AAA GCA GAT GCA AGT AGT CTG GAC AAA TAT TTA ACT GAA	923
Glu Gly Asn Lys Ala Asp Ala Ser Ser Leu Asp Lys Tyr Leu Thr Glu	
25 30 35 40	
AGT CAG TTT CAT GAT AAA CGC ATA GCA GAA GAA TTA AGA ACT TTA CTT	971
Ser Gln Phe His Asp Lys Arg Ile Ala Glu Glu Leu Arg Thr Leu Leu	
45 50 55	

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AAC AAA TCG AAT GTA TAT GCA TTA GCT GCA GGA AGC TT 1009  
Asn Lys Ser Asn Val Tyr Ala Leu Ala Ala Gly Ser  
60 65

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 781 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAGATAACT ATATTTTGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA 60  
TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA 120  
TTAACATGAA AAATAAATTG ATAGCAAAAT CTTTATTAAC AATAGCGGCA ATTGGTATTA 180  
CTACAAC TAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA 240  
AACCAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT 300  
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT 360  
TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG 420  
CGAAAACTGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA 480  
GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT 540  
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT 600  
TAAAACAAGG ATTAGTGAGA TAATACTTCT GTCATTATTT TAAGTTCAAA ATAATTTAAT 660  
ATTATATTAT TTTTATTAA TAAAACGACT ATGCTATTTA ATGCCAGGTT AATGTAACTT 720  
TCCTAAAATT GACTATATAA TCGTTAAGTA TCAATTTTAA GGAGAGTTTA CAATGAAATT 780  
T 781

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAGATAGCT ATATTCAGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA	60
TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA	120
TTGACATGAA AAATGCATTG ATAGCAAAAT CTTTATTAAC ATTAGCGGCA ATAGGTATTA	180
CTACAACCTAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA	240
AACCAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT	300
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT	360
TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG	420
CGAAAACCTGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA	480
GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT	540
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT	600
TAAAACAAGG ATTAGTTAAA TAAAACTTCA ATCGTTGCTG TTATCTGGAA ATAATTAATT	660
AAATGTTATG TTAATTTTTG TTAATGAAAA AAGTAATCTA TTTAATGACA GGTAAATGTA	720
ATTGTCCTGA AATTGACTAT ATACTCAGTA AGTATCAATT TTAAGGAGAG CTTATAATGA	780
AATTT	785

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Lys	Asn	Lys	Leu	Ile	Ala	Lys	Ser	Leu	Leu	Thr	Ile	Ala	Ala	Ile
1				5					10					15	
Gly	Ile	Thr	Thr	Thr	Thr	Ile	Ala	Ser	Thr	Ala	Asp	Ala	Ser	Glu	Gly
			20					25					30		
Tyr	Gly	Pro	Arg	Glu	Lys	Lys	Pro	Val	Ser	Ile	Asn	His	Asn	Ile	Val
		35					40					45			



Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn  
50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu  
65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys  
85 90 95

Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile  
100 105 110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser  
115 120 125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr  
130 135 140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys  
145 150 155 160

Gln Gly Leu Val Arg  
165

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Asn Ala Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile  
1 5 10 15

Gly Ile Thr Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly  
20 25 30

Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val  
35 40 45

Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn  
50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu  
65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys  
85 90 95

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(2) INFORMATION FOR SEQ ID NO:14:

(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Glu	Gly	Tyr	Gly	Pro	Arg	Glu	Lys	Lys	Pro	Val	Ser	Ile	Asn	His
1				5					10					15	
Asn	Ile	Val	Glu	Tyr	Asn	Asp	Gly	Ser	Phe	Lys	Tyr	Gln	Ser	Arg	Pro
			20					25					30		
Lys	Phe	Asn	Ser	Thr	Pro	Lys	Tyr	Ile	Lys	Phe	Lys	His	Asp	Tyr	Asn
		35					40					45			
Ile	Leu	Glu	Phe	Asn	Asp	Gly	Thr	Phe	Glu	Tyr	Gly	Ala	Arg	Pro	Gln
	50					55					60				
Phe	Asn	Lys	Pro	Ala	Ala	Lys	Thr	Asp	Ala	Thr	Ile	Lys	Lys	Glu	Gln
65					70					75					80
Lys	Leu	Ile	Gln	Ala	Gln	Asn	Leu	Val	Arg	Glu	Phe	Glu	Lys	Thr	His
				85					90					95	
Thr	Val	Ser	Ala	His	Arg	Lys	Ala	Gln	Lys	Ala	Val	Asn	Leu	Val	Ser
			100					105					110		
Phe	Glu	Tyr	Lys	Val	Lys	Lys	Met	Val	Leu	Gln	Glu	Arg	Ile	Asp	Asn
		115					120					125			
Val	Leu	Lys	Gln	Gly	Leu	Val	Arg								
	130						135								

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Ser Gln Tyr Gly Pro Arg Pro Gln Phe Asn Lys Thr Pro Lys Tyr  
1 5 10 15  
Val Lys Tyr Arg Asp Ala Gly Thr Gly Ile Arg Glu Tyr Asn Asp Gly  
20 25 30  
Thr Phe Gly Tyr Glu Ala Arg Pro Arg Phe Asn Lys Pro Ser Glu Thr  
35 40 45  
Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly  
50 55 60  
Ala Arg Pro Thr Tyr Lys Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val  
65 70 75 80  
Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Gln  
85 90 95  
Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val Thr Thr His Gly Asn  
100 105 110  
Gly Gln Val Ser Tyr Gly Ala Arg Gln Ala Gln Asn Lys Pro Ser Lys  
115 120 125  
Thr Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr  
130 135 140  
Gly Ala Arg Pro Thr Tyr Lys Lys Pro Ser Lys Thr Asn Ala Tyr Asn  
145 150 155 160  
Val Thr Thr His Ala Asp Gly Thr Ala Thr Tyr Gly Pro Arg Val Thr  
165 170 175  
Lys

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